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1/58

PCT/JP98/04475

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## Sequence Listing

(110) Sagami Chemical Research Center

5 (120)

· 130 · 660856

• 140 •

10 141

· 150 · Japan 9-276271

.151 1997-10-08

15 160 40

<170> Windows 95 (Word 98)

(210) 1

211 - 122

20 212c PRT

1213 *Homo sapiens*

3400

#### REFERENCES AND NOTES

Die ersten drei Minuten der Sitzung werden für die Begrüßung und die Vorstellung der Teilnehmer reserviert.

Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu Gly Glu Gln Cys

35

40

45

--

Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys

50

55

60

5 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly

65

70

75

80

Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly

85

90

95

Ala His Ala Leu Gin Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala

10

100

105

110

Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu

115

120

15 '210' 2

'211' 220

'212' PRT

'213' Homo sapiens

20 '400' 2

Met Ser Met Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly

1

5

10

15

Trp Leu Gly Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser

35

40

45

50                    55                    60  
Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg --  
65                    70                    75                    80  
Ala Leu Ile Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val  
5                    85                    90                    95  
Ala Leu Val Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala  
100                  105                  110  
Lys Ala Lys Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala  
115                  120                  125  
10    Leu Leu Thr Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg  
130                  135                  140  
Asp Phe Tyr Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly  
145                  150                  155                  160  
Ala Gly Leu Tyr Val Gly Trp Ala Ala Ala Leu Gln Leu Leu Gly  
15                  165                  170                  175  
15                  165                  170                  175  
Gly Ala Leu Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Tyr Thr  
180                  185                  190  
Ala Thr Lys Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala  
195                  200                  205  
20    Ser Leu Gly Thr Gly Tyr Asp Arg Lys Asp Ile Val  
210                  215                  220

&lt;400&gt; 3

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val Phe

1 5 10 15

5 Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly Pro

20 25 30

Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys Cys

35 40 45

Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Leu Phe

10 50 55 60

Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His Trp

65 70 75 80

Pro

15

&lt;210&gt; 4

&lt;211&gt; 301

&lt;212&gt; PRT

213) homo sapiens

20

&lt;400&gt; 4

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg Gly

1 5 10 15

Ala Leu Leu Pro Ile Val Ile Asp Asp Leu Gly Tyr Leu Ala Leu Arg

Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile Gly  
50 55 60 --

Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro Ala  
65 70 75 80

5 Ala Gly Ala Gly Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly Pro  
85 90 95

Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn Met  
100 105 110

Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu He  
10 115 120 125

Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala Gly  
130 135 140

Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn Gln  
145 150 155 160

15 Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile Leu  
165 170 175

Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro Val  
180 185 190

Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala Ala  
20 195 200 205

Val Phe Tyr Val Arg Tyr Arg Thr Leu Pro Thr Pro Arg Thr Leu Ala  
210 215 220

Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr Phe

260

265

270

Leu Trp Cys Phe Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser Tyr

—

275

280

285

Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp

5 290

295

300

· 210 · 5

· 211 · 383

10 · 212 · PRT

· 213 · Homo sapiens

· 400 · 5

Met Glu Ala Leu Gly Lys Leu Lys Gln Phe Asp Ala Tyr Pro Lys Thr

15 1 5 10 15

Leu Glu Asp Phe Arg Val Lys Thr Cys Gly Gly Ala Thr Val Thr Ile

20

25

30

Val Ser Gly Leu Leu Met Leu Leu Leu Phe Leu Ser Glu Leu Gln Tyr

35

40

45

20 Tyr Leu Thr Thr Glu Val His Pro Glu Leu Tyr Val Asp Lys Ser Arg

50

55

60

Gly Asp Lys Leu Lys Ile Asn Ile Asp Val Leu Phe Pro His Met Pro

65

70

75

80

Leu Asp Val Glu His Asn Ile Phe Lys Gln Arg Leu Asp Lys Asp Gly

Ile Pro Val Ser Ser Glu Ala Glu Arg His Glu Leu Gly Lys Val Glu  
115 120 125 —  
Val Thr Val Phe Asp Pro Asp Ser Leu Asp Pro Asp Arg Cys Glu Ser  
130 135 140  
5 Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys Cys Cys Asn Thr Cys Glu  
145 150 155 160  
Asp Val Arg Glu Ala Tyr Arg Arg Gly Trp Ala Phe Lys Asn Pro  
165 170 175  
Asp Thr Ile Glu Glu Cys Arg Arg Glu Gly Phe Ser Gln Lys Met Gln  
180 185 190  
10 Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr Gly Phe Leu Glu Val Asn  
195 200 205  
Lys Val Ala Gly Asn Phe His Phe Ala Pro Gly Lys Ser Phe Gln Gln  
210 215 220  
15 Ser His Val His Val His Asp Leu Gln Ser Phe Gly Leu Asp Asn Ile  
225 230 235 240  
Asn Met Thr His Tyr Ile Gln His Leu Ser Phe Gly Glu Asp Tyr Pro  
245 250 255  
Gly Ile Val Asn Pro Leu Asp His Thr Asn Val Thr Ala Pro Gln Ala  
260 265 270  
20 Ser Met Met Phe Gln Tyr Phe Val Lys Val Val Pro Thr Val Tyr Met  
275 280 285  
Lys Val Asp Gly Glu Val Leu Arg Thr Asn Gln Phe Ser Val Thr Arg  
295 300 305 310  
315 320

325                    330                    335

Lys His Arg Ser Phe Thr His Phe Leu Thr Gly Val Cys Ala Ile Ile

340                    345                    350

Gly Gly Met Phe Thr Val Ala Gly Leu Ile Asp Ser Leu Ile Tyr His

5                    355                    360                    365

Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp Leu Gly Lys Thr Thr

370                    375                    380

10                    210                    216

211                    199

212                    PRT

213                    Homo sapiens

15                    3400                    3406

Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp Pro Ser Phe Val

1                    5                    10                    15

Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr Trp Asn Val Val

26                    25                    30

20                    Ala Arg Trp Glu His Iys Thr Arg Lys Leu Ser Arg Ala Phe Gly Ser

35                    40                    45

Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile Leu Leu Leu Asn

50                    55                    60

Met Ala Ser Ile Ile Asp Thr Ile Ala Val Ile Ser Leu Gly Leu Ala Ile

Leu Gly Leu Gly Val Val Leu Val Ser Ser Phe Phe Ala Leu Gly

100

105

110

Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile Leu Lys Glu Ala

115

120

125

5 Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn Pro Met Tyr Trp

130

135

140

Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met His Ala Ser Pro

145

150

155

160

Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr Tyr Ile Val Ala

10

165

170

175

Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr Arg Gln Lys Ala

180

185

190

Ser Gly Ser His Lys Arg Ser

195

15

<210> 7

<211> 229

<212> PRT

20 <213> Homo sapiens

<400> 7

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Ile Val Pro Trp Ala

35                    40                    45

Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala Arg Cys —

50                    55                    60

Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln Asn Cys

5     65                    70                    75                    80

Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr Thr Val

85                    90                    95

Ile Ile Asp Leu Gln Ala Asn Pro Leu Lys Gly Asp Leu Ala Asn Thr

100                    105                    110

10 Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln His Val

115                    120                    125

Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser Tyr Ile

130                    135                    140

Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn Thr Gly

15 145                    150                    155                    160

Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp Gly Pro

165                    170                    175

Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr Lys Cys

180                    185                    190

20 Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Ile Gly Ile Leu Gly

195                    200                    205

Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln Arg Arg

210                    215                    220

&lt;210&gt; 8

&lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

**5**

&lt;400&gt; 8

Met Ser Pro Ser Gly Arg Leu Cys Leu Leu Thr Ile Val Gly Leu Ile

1 5 10 15

Leu Pro Thr Arg Gly Gln Thr Leu Lys Asp Thr Thr Ser Ser Ser

10 20 25 30

Ala Asp Ser Thr Ile Met Asp Ile Gln Val Pro Thr Arg Ala Pro Asp

35 40 45

Ala Val Tyr Thr Glu Leu Gln Pro Thr Ser Pro Thr Pro Trp Pro

50 55 60

15 Ala Asp Glu Thr Pro Gln Pro Gln Thr Gln Gln Leu Glu Gly

65 70 75 80

Thr Asp Gly Pro Leu Val Thr Asp Pro Glu Thr His Lys Ser Thr Lys

85 90 95

Ala Ala His Pro Thr Asp Asp Thr Thr Ser Leu Ser Glu Arg Pro Ser

20 100 105 110

Pro Ser Thr Asp Val Gln Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly

115 120 125

Phe His Glu Asp Asp Pro Phe Phe Tyr Asp Glu His Thr Leu Arg Lys

145 150 155 160

165

170

175

Cys Arg

5 (210) 9

(211) 443

(212) PRT

(213) Homo sapiens

10 (400) 9

Met Arg Leu Thr Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr

1

5

10

15

Cys Leu Phe Ser Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg

20

25

30

15 Arg Gln Ala Pro Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala

35

40

45

Pro Ala Arg Glu Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu

50

55

60

Glu Trp Asn Pro Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg

20 65

70

75

80

Phe Lys Thr Ser Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr

85

90

95

Asp Leu Ser Val Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu

115

120

125

130                    135                    140  
Ile Thr Gly Pro Ala Val Ile Pro Gly Tyr Phe Ser Val Asp Val Asn  
145                    150                    155                    160  
Asn Val Val Leu Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr  
5                      165                    170                    175  
Ala Thr Gln Trp Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys  
180                    185                    190  
Leu Gln His Leu Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn  
195                    200                    205  
10        Glu Trp Ile Asn Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu  
210                    215                    220  
Leu Phe Ile Ile Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe  
225                    230                    235                    240  
Gln Trp Pro Leu Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu  
15                      245                    250                    255  
Ala Ser Trp Ser Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe  
260                    265                    270  
Leu Gly Thr Ile Tyr Glu Asn Ser Ser Arg Gin Ala Leu Met Asn Ile  
275                    280                    285  
20        Leu Lys Lys Asp Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu  
290                    295                    300  
His Trp Gln Pro Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp  
305                    310                    315                    320  
Ile Asn Ile Arg Ile Ile Ile Ala Cys Ser Ile Gly Ser Ile Pro Val

Val Glu Asp Val Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His

355

360

365

--

His Gly Ala Pro Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile

370

375

380

5 Phe Ile Lys Asn Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys

385

390

395

400

Thr Ile Ile Leu Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln

405

410

415

Trp Tyr Gln His Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile

10

420

425

430

Leu Glu Ser Ser Phe Leu Met Asn Asn Lys Ser

435

440

15 <210> 10

<211> 130

<212> PRT

<213> Homo sapiens

20 <400> 10

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Ser

1

5

10

15

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu

50                    55                    60  
Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln Ser  
65                    70                    75                    80  
Glu Asp Lys Arg Glu Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg  
5                    85                    90                    95  
Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly Leu  
100                  105                  110  
Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser Thr  
115                  120                  125  
10 Val Met  
130  
  
(210) 11  
15 (211) 369  
(212) DNA  
(213) Homo sapiens  
  
400 11  
20 atgaagggtg tgcgtgttgc cctgttgtatg gcagggtttgg ccctgcggcc agggactgcc         60  
ctgtgtgtgt actcctgcaa agccccagggtg agcaacgagg actgcctgca ggtgaagaac         120  
tgcacccca ggggggagca gtgtgtggacc ggcgcgcattc ggcgcgtttgg ctcctgtacc         180  
gtcatcagca aaggctgcag cttgaactgc gtggatgact cacaggacta ctacgtggc         240

210 > 12

211, 660

· 212 · DNA

5 213 *Homo sapiens*

<400> 12

atgtccatgg gcctggagat caccggcacc gegetggccg tgctgggcgc acggggacc 60

**10** acgtcgaga acatctggga gggcttgtgg atgaactgcg tggcgcagag caccggccag

atgcagtgtaca aggtgtacga ctccgcggcg gcaactggccac aggaccccta atccatcccccc 310

gccccatcg tggtggccat ccgtgtggcc gcccgtggcc tgcgtatggc gatggatggc 300

assaltateggia la saetta, la saetta assalta l'assalto, l'assalto assalta l'assalto.

искусств, заложила основу для дальнейшего развития японской культуры.

Изложена классическая связь между классической и квантовой механикой.

20

210 · 13

211 > 213

## (212) DNA

ggttttttgg tgccttggtt cattccataag ggttcataacc ggggagttat cattaccatg 120  
 ttggtgacct gttcagtttgc tgcataatc ttttggcgta tttcaatttc gcccactc 180  
 aacccttcctt ttggacccgca attaaaaat gaaaccatct ggtatctgaa gtatcattgg 240  
 cct  
 243

5

&lt;210&gt; 14

&lt;211&gt; 903

&lt;212&gt; DNA

10 &lt;213&gt; Homo sapiens

&lt;400&gt; 14

atgcttagct tgcgcgtggc gcgcggctcg tggggggccc tgcgcggcgc cgcttgggt 60  
 ccgggaacgc ggccgagtaa gcgacgcgcc tgcgtggccc tgcgtccgc cgtccccctgc 120  
 15 tgcttgggt gcctggccga acgctggagg ctgcgtccgg ccgcctttgg cttggggctg 180  
 ccgggatcg gccagcggaa ccactgttcg ggcggggga aggccggctcc caggccagcg 240  
 gccggagcgg ggcggcgtgc cgaagccccg ggcggccagt gggggccggc gagcaccccc 300  
 agcctgtatg aaaacccatg gacaateccg aataatgttgc caatgacgag aattggcttg 360  
 gccccatgtt tgggttattt gattattgaa gaagattttta atattgcattt aggagttttt 420  
 20 gctttagctg gactaacaga ttgttggat ggatttttg ctgcggactg ggcacatcaa 480  
 agatcagttt tggaaagtgc ttttgcataa cttgtgtata aaatacttat cagtatctta 540  
 tatgttagct tgacctatgc agatctttt ccgttccaa ttacttaat gtcattttgg 600  
 agagatctaa tgggttggatgc tgcgtttttt tatgtcagat acggaaactt tccaaacacca 660  
 gttttttttt atgtgtacatg cttttttttt cagatctatg ggtgtttttt aatgtttttgg 840

gac

903

(210) 15

5 211 · 1149

212 · DNA

· 213 Homo sapiens

(400) 15

10 atggaggegc tggggaaatc gaagcaggtc gatgcctacc ccaagacttt ggaggacttc 60  
cgggtaaga cctgcggggg cgcacccgtg accatgtca gtggccttct catgtgtcta 120  
ctgttctgt ccgagctgca gtattacetc accacggagg tgcatectga getctacgtg 180  
gacaagtgcg ggggagataa actgaagata aacatcgatg tacttttcc gcacatgect 240  
tgtgcctata ttagtattga tgccatggat gtggccggag aacagcagct ggatgtggaa 300  
15 cacaacctgt tcaagcaacg actagataaa gatggcatcc cctgtgagctc agaggttgag 360  
cggtcatgagc ttggaaagt cgaggtgacg gtgtttgacc ctgactccct ggaccttgat 420  
cgctgtgaga getgttatgg tgetgaggca gaagatatac agtgcgttaa cacctgtgaa 480  
gatgtgcggg aggcatactcg cctgtgaggc tggccttca agaaccctaga tactatttag 540  
cagtgcggc gagagggctt cagccagaag atgcaggagc agaagaatga aggtgtccag 600  
20 gtgtatggc ttttggaaatc caataagggtg gcccggaaact tccacttttc ccttggaaag 660  
agtttccatc agtccccatgt gcacgtccat gacttgcaga gctttggct tgacaacatc 720  
aacatgaccc actacatcca gcaactgtca tttggggagg actatccagg cattgtgaac 780  
cccttggacc acaccaatgt cactgtggcc caagccctca tgcatttccat gtactttgtg 840

gttttgcgtt tttatgtt ctttgcgttttgcgtt gttttggggatc tggggggatc gttttggggatc tggggggatc

ctcatcgatt cgctcatcta ccactcagca cggccatcc agaagaaaat tgcgttaggg 1140  
aagacaacg 1149

5 210> 16

211> 597

212> DNA

213> Homo sapiens

10 > 400> 16

atgaccggc tgcgtggctt cgtggacccc ctggatccaa gttttgtggc tgcgtcate 60

accatcacct tcaatccgtt ctactggaaat gtggttgcac gatggaaaca caagaccgc 120

aagctgagca ggcccttggg atccccctac cttggctgtt acttcataag cgtcaccatc 180

ctgctcttga acttccttgcg ctgcactgc ttcaacgcagg ccatgttgag ccagccagg 240

15 atggagagcc tggacacccc cggggcttac agcttggcc tggcgctctt gggactggc 300

gtcgtgtctcg tgcgtccat ctttttgcg ctgggttgcg ctggaaatcccttaggtat 360

tacttggga ttcgtcaagga gggagagtg accgtgttcc cttcaacat cttggacaa 420

ccatgtact gggaaagcac agccaaatccat cttgggttggg ccataatgcg cggccatccc 480

atggggctgc ttcgtacggt gtcgtggcc ctccatccat tttgtgttcc cttatacgaa 540

20 gggccatcca cccgtggat cttccggcag aaaggcttgcg ggtttccatccaa gagggac 597

> 210> 17

〈400〉 17

	atggcgcctc acggcccgaa tagtcttaag accctgggtgc cctgggatgc cgccctgttc	60
	cctcgatctgg gctgtggaaag ggctctggcg ctacccgaga tatgcaccca atgtccagg	120
	agcgtgcaaa atttgtcaaa agtggccttt tattgtaaaa cgacacgaga gctaatagtcg	180
5	catgcccgtt gctgcctgaa tcagaaggc accatcttgg ggctggatct ccagaactgt	240
	tctctggagg accctggtcc aaactttcat caggcacata ccactgtcat catagacctg	300
	caagcaaacc ccctcaaagg tgacttggcc aacaccccttc gtggctttac tcagctccag	360
	actctgtatac tgccacaaca tgtcaactgt cctggaggaa ttaatgcctg gaataactatc	420
	accctttata tagacaacca aatctgtcaa gggcaaaaga acccttgcaa taacactggg	480
10	gaccctggaaa tgtgtcttga gaatggatct tggttacctg atggccagg tcttttgcag	540
	tgtgttttgtc cttatggttt ccatggatac aagtgtatgc gccagggttc gtttctcaactg	600
	tttatgtttt tgggatctt gggagccacc acctatccg tttccattctt gttttggcgt	660
	acccagcgcc gaaaagccaa gacttca	687

15

(210) 18

211 > 534

(212) DNA

213 *Homo sapiens*

20

400 18

atgtcgcct ctggtegcct gtgttcttc accatcgttg gcttgatttc cccacccaga 60  
ggacagacgt taaagatac caagtccagt ttccagcag actcaactat catggacatt 120

ccccagaccc tcaagccatc tggtttcat gaggatgacc ccttcttcta tgatgaacac 420  
accctccgga aacggggct gttggtcga ctgtgtgttcatcacagg catcatcate 480  
etcaccatgc gcaagtgcag gcagctgtcc cggatatgcc ggaatcattg cagg 534

5

210> 19

211 1329

· 212 > DNA

213 Homo sapiens

10

(400) 19

```

atggggctga cgccggaaacgcg gtcgttgtcg ttttttttatacg ccctgtactg cctatttcac 60
ctctaacgtg cctaccacgt cttttttgggg cgccggccgcg aggccggcggc cgggtcccccg 120
cggggcctca ggaaggggggc ggccccccgcg cgggagagac gggccgcaga acagtccact 180

```

15 ttggaaatgt aagaatggaa tcccttggaa ggagatgaaa aataatgacca acacacacaa

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ttaaaaacta gcccgtcaaat attagataaaa tccacgaaag gaaaaacaga ttcgtgtat 300
caaatctggg gcaaaggctgc cattggcttg tatctctggg agcataatttt tgaaggctta 360
cttgatecca gegatgtgac tgcgtcaatgg agagaaggaa agtcaatcgt aggaaagaaca 420
cagtacatgt tcataactgg tccatgtgtat acccagggt acgttcgtt tgcgtgtat 480

```

20 aatgtggtagtattttaaa tggaaaggagg aaggcaaaaat ttttttttc cccatgc

```

ttactttatg caaaaattt agtgeaaatt caaaaacttc agcatcttgc tgggttttg 600
ctcgaaatg aacattgtga taatgagtgg ataaacccat tcctcaaaag aatggagge 660
tttgtggage tggttttcat aatataatgac agccctggta taatgaact ggatgtttt 720

```

<sup>1</sup> See also the discussion of the relationship between the two in the section on "Theoretical Approaches" above.

gccttgcctc agagtgtatc cacattgtgc cgggtggag taaacacaga atgttatcga 1020  
atctatgagg ctgttccta tggctccatt cctgtgggtgg aagacgtat gacagctggc 1080  
aactgtggga atacatctgt gcaccacggt gtcctctgc agttatcaa gtccatgggt 1140  
gtccctta tctttatcaa gaactggaag gaacctcccg ctgttttaga aaaagagaaa 1200  
5 actataattt tacaagaaaa aatttgaaga agaaaaatgt tacttcaatg gtatcagcac 1260  
ttcaagacag agcttaaaat gaaattttact aatatttttag aaagtcatt ttatgaat 1320  
aataaaaagt 1329

10 <210> 20

<211> 390

<212> DNA

<213> Homo sapiens

15 <400> 20

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gttggggacg aggaggagac catgttcaatggatccaa acatataccaa ggaccagat 240  
20 gaagacauaa gagagaagaa agagggttag gagaagaag agaaggggaa gaaggagaaa 300  
aagacaccaa aggaaggaga gagcaacttg ggactggatc tggaggaaaa agaccccgaa 360  
gaccatgaga gagcaaaagag cacagtcatg 390

213 Homo sapiens

〈400〉 21

agccaccacg tgacc atg aag gct gtg ctg ctt gcc ctg ttg atg gca ggc 51

5 Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly

1                        5                        10

ttg gcc ctg cag cca ggc act gcc ctg ctg tgc tac tcc tgc aaa gcc 99

Leu Ala Leu Gln Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala

10 cag gtg agc aac gag gac tgc ctg cag gtg aag aac tgc aca cag ctg 147

Gln Val Ser Asn Glu Asp Cys Leu Gln Val Lys Asn Asp Cys Thr Gln Leu

ggg gag cag tgc tgg acc gcg cgc atc cgc gca gtt ggc ctc ctg acc 195

Gly Glu Gln Cys Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr

15      45      50      55      60

gtc atc agg aaa ggc tgc agg tgg aac tgc gtc gag tac tca cca gac 313

Val Ile Ser Lys Gly Cys Ser Leu Asp Cys Val Asp Asp Ser Gln Asp

65 70 75

lac lac-gtg-ggc-aag-aaa-aaa-atc-acg-lac-lac lac lac lac lac lac lac 291

20 Tyr Tyr Val Glu Lys Lys Asn Ile Thr Cys Lys Asp Thr Asp Ile Cys

80                    85                    90

aac gcc agc egg gcs cat gcc sig gag cgg gct gcc gcc alc cut tea 329

Asn-Ala-Ser-Gly-Ala-His-Ala-Leu-Gln-Pro-Ala-Ala-Ala-Lys-Lys-Ala

Digitized by srujanika@gmail.com

	tagget ctggggggcc cgcgtgcage ccacactggg tgggtgccc caggcctctg	440
	tgcacactt cacagacctg gcccagtggg agcctgtctt ggttccctgag gcacatctta	500
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5	cctccaaacc tctctgtctgc tggttccatg gcccagcatt ctccacccctt aaccctgtgc	680
	tcaggcacct ttccccccag gaagecttcc ctgcccaccc catctatgac ttgagccagg	740
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	ggctgagatg aagtggactg agtagaactg gaggacaaga gtcgacgtga gtctctggga	860
	gtctccagag atggggccctg gagggcttggaa ggaaggggccc aggccctcaca ttctgtgggc	920
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· 210&gt; 22

&lt;211&gt; 123

15 &lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 22

Met Lys Ala Val Leu Ieu Ala Leu Leu Met Ala Gly

20 1 5 10

Leu Ala Leu Gln Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala

15 20 25

Gln Val Ser Asn Glu Asp Cys Leu Gln Val Lys Asn Cys Thr Gln Leu

45

50

55

60

22

65                    70                    75  
Tyr Tyr Val Gly Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys  
80                    85                    90  
Asn Ala Ser Gly Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala  
5                    95                    100                    105  
Leu Leu Pro Ala Leu Gly Leu Leu Trp Gly Pro Gly Gln Leu  
110                    115                    120  
  
10 <210> 23  
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<212> DNA  
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ccgtccgtcc gtcggggcgc cgcagtccc gccaggccca gggccccgg ccctctgtct        180  
cccgccaccc ggagccaccc ggtggagccgg gacttgcgc ggcagcc atg tcc atg        236  
20                    Met Ser Met  
:  
ggc ctg gag atc acg ggc acc ggc cgg gcc ggg ctg ggc tgg ctg ggc        284  
Gly Leu Glu Ile Thr Gly Thr Ala Leu Ala Val Leu Gly Trp Leu Gly

Ile Ile Val Ile Lys Alanine Pro Met Trp Arg Val Ser Ile Ile Ile

ggc agc aac atc atc acg tcg cag aac atc tgg gag ggc ctg tgg atg 380  
Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly Leu Trp Met —  
40 45 50

aac tgc gtg gtg cag aac acc ggc cag atg cag tgc aag gtg tac gac 428  
5 Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp  
55 60 65

tcg ctg ctg gca ctg cca cag gac ctt cag gcg gcc cgc gcc ctc atc 476  
Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Ile  
70 75 80

10 gtg gtg gcc atc ctg ctg gcc gcc ttc ggg ctg cta gtg gcg ctg gtg 524  
Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala Leu Val  
85 90 95

ggc gcc cag tgc acc aac tgc gtg cag gac gac acg gcc aag gcc aag 572  
Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys  
15 100 105 110 115

atc acc atc gtg gca ggc gtg ctg ttc ctt ctc gcc gcc ctg ctc acc 620  
Ile Thr Ile Val Ala Gly Val Phe Leu Leu Ala Ala Leu Leu Thr  
120 125 130

ctc gtg ccc gtg tcc tgg tcc gac aac acc att atc egg gac ttc tac 668  
20 Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr  
135 140 145

aac ccc gtg gtg ccc gag gcg cag aag cgg gag atg ggc gcg ggc ctg 716  
Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly Ala Gly Leu

Ile Val Val Val Ala Ala Ala Leu Gln Ile Val Gly Gly Ala Leu

ctc tgc tgc tcg tgt ccc cca cgc gag aag aag tac aeg gcc acc aag 812  
Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys  
180 185 190 195

gtc gtc tac tcc gcg ccg cgc tcc acc ggc ccg gga gcc agc ctg ggc 860  
5 Val Val Tyr Ser Ala Pro Arg Ser Thr Gly Pro Gly Ala Ser Leu Gly  
200 205 210

aca ggc tac gac cgc aag gac tac gtc taa gggacagacg cagggagacc 910  
Thr Gly Tyr Asp Arg Lys Asp Tyr Val  
215 220

10 ccaccaccac caccaccacc aacaccacca ccaccacage gagctggage ggcaccagg 970  
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15 ggcctggca gggacggca gcccctggaang gggcaatttgc ttttttcaa taaaaggctt 1150  
tctttttgc 1210  
1270  
1279

&lt;210&gt; 24

20 &lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

5                    10                    15

Thr Ile Val Cys Cys Ala Leu Pro Met Trp Arg Val Ser Ala Phe Ile  
20                    25                    30                    35

Gly Ser Asn Ile Ile Thr Ser Gln Asn Ile Trp Glu Gly Leu Trp Met  
5                    40                    45                    50

Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys Lys Val Tyr Asp  
55                    60                    65

Ser Leu Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala Arg Ala Leu Ile  
70                    75                    80

10    Val Val Ala Ile Leu Leu Ala Ala Phe Gly Leu Leu Val Ala Leu Val  
85                    90                    95

Gly Ala Gln Cys Thr Asn Cys Val Gln Asp Asp Thr Ala Lys Ala Lys  
100                  105                  110                  115

Ile Thr Ile Val Ala Gly Val Leu Phe Leu Leu Ala Ala Leu Leu Thr  
115                  120                  125                  130

Leu Val Pro Val Ser Trp Ser Ala Asn Thr Ile Ile Arg Asp Phe Tyr  
135                  140                  145

Asn Pro Val Val Pro Glu Ala Gln Lys Arg Glu Met Gly Ala Gly Leu  
150                  155                  160

20    Tyr Val Gly Trp Ala Ala Ala Leu Gln Leu Leu Gly Gly Ala Leu  
165                  170                  175

Leu Cys Cys Ser Cys Pro Pro Arg Glu Lys Lys Tyr Thr Ala Thr Lys  
180                  185                  190                  195

Lys Lys Tyr Thr Ala Thr Lys

&lt;210&gt; 25

&lt;211&gt; 835

5 &lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

gacacttcct ggtgggatcc gagtgaggcgc acggggtagg ggttggcgct caggcggcga 60

10 cc atg gcg tat cac ggc ctc act gtg cct ctc att gtg atg agc gtg 107

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val

1 5 10 15

ttc tgg ggc ttc gtc ggc ttc ttg gtg cct tgg ttc atc cct aag ggt 155

Phe Trp Gly Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly

15 20 25 30

cct aac cgg gga gtt atc att acc atg ttg gtg acc tgt tca gtt tgc 263

Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys

35 40 45

tgt tat ctc ttt tgg ctg att gca att ctg gaa caa ctc aac ctc ctc 251

20 Cys Tyr Leu Phe Trp Leu Ile Ala Ile Leu Ala Gln Leu Asn Pro Iou

50 55 60

ttt gga ccc caa ttg aaa aat gaa acc atc tgg tat ctg aag tat cat 299

Phe Gly Pro Gln Leu Lys Asn Glu Thr Ile Trp Tyr Leu Lys Tyr His

170 171

agaagagaat gccttctaga tgcaaaatca cctccaaacc agaccacttt tcttgacttg 410  
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atgcagcgtg tttcctttg cctttttgc actttggta attacgtgcc tccataacct 530  
gaactgtgcc gactccacaa aacgattatg tactcttcgt agatagaaga tgctgttctt 590  
5 ctgagagata cgttactctc tccttggaaat ctgtggattt gaagatggct cctgccttct 650  
cacgtggaa tcagtgaagt gtttagaaac tgetgcaaga caaacaagac tccagtgccc 710  
tggtcagtag gagagcacgt tcagaggaa gagccatctc aacagaatcg caccaaacta 770  
tactttcagg atgaatttct tcttctgcc atcttttggaa ataaatatattt tcctccttctc 830  
tatgg 835

10

210 26

211 81

212 PRT

15 213 Homo sapiens

2400 26

Met Ala Tyr His Gly Leu Thr Val Pro Leu Ile Val Met Ser Val

1

5

10

15

20 Phe Trp Giv Phe Val Gly Phe Leu Val Pro Trp Phe Ile Pro Lys Gly

20

25

30

Pro Asn Arg Gly Val Ile Ile Thr Met Leu Val Thr Cys Ser Val Cys

35

40

45

Phe Giv Pro Gln Leu Iys Asn Glu Ile Ile Trp Tyr Leu Lys Tyr His

Trp Pro

80

5 &lt;210&gt; 27

&lt;211&gt; 1256

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

10 &lt;400&gt; 27

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ctcgccatgt tcccaaggctg ctgagetetc gcccgcggag accccgcggc gccccggcag 120  
ggcc atg cta gcc ttg cgc gtg gcg cgc ggc tcg tgg ggg gcc ctg cgc 169  
Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg

15 1 5 10 15

ggc gac get tgg get ccg gga acg cgg ccg agt aag cga cgc gcc tgc 217  
Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys

20 20 25 30

tgg gac ctg ctg cgg ccc gtg ccc tgc tgc ttg ggc tgc ctg gac gaa 265

20 Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu

35 35 40 45

cgc tgg agg ctg cgt cgg gac get ctt ggc ttg egg ctg ccc ggg atc 313  
Arg Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile

Gly Gln Arg Asn His Ile Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro

gct gcc gca gct ggc gtc gct gca gaa gtc ccc ggc ggc cag tgg ggc 409  
Ala Ala Gly Ala Gly Ala Ala Ala Glu Ala Ala Pro Gly Gly Gln Trp Gly  
80 85 90 95

ccg gct aac acc ccc aac ctc ctg tat gaa aac cca tgg aca atc ccg aat 457  
5 Pro Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn  
100 105 110

atg ttg tca atg aeg aga att ggc ttg gcc cca gtt ctg ggc tat ttg 505  
Met Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu  
115 120 125

att att gaa gaa gat ttt aat att gca cta gga gtt ttt gct tta get 553  
10 Ile Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala  
130 135 140

gga cta aca gat ttg gat gga ttt att gct cga aac tgg gcc aat 601  
Gly Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn  
15 145 150 155

caa aga tca gct ttg gga agt gct ctt gat cca ctt gct gat aaa ata 649  
Gln Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile  
160 165 170 175

ctt atc agt ate tta tat gtt aac ttg aac tat gca gat ctt att cca 687  
20 Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro  
180 185 190

ggt cca ctt act tac atg aac att tgg aac gat gta atg ttg att gct 745  
Val Pro Leu Thr Tyr Met Ile Ile Ser Arg Asp Val Met Leu Ile Ala

Met Val Phe Tyr Val Arg Tyr Arg Ile Leu Tyr Thr Pro Arg Thr Leu

gcc aag tat ttc aat cct tgc tat gcc act get agg tta aaa cca aca 841  
Ala Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Ileu Lys Pro Thr --  
225 230 235  
ttc atc agc aag gtg aat aca gca gtc cag tta atc ttg gtg gca gct 889  
5 Phe Ile Ser Lys Val Asn Thr Ala Val Gln Leu Ile Leu Val Ala Ala  
240 245 250 255  
tct ttg gca gct cca gtt ttc aac tat gct gac agc att tat ctt cag 937  
Ser Leu Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Gln  
260 265 270  
10 ata cta tgg tgt ttt aca get ttc acc aca get gca tca get tat agt 985  
Ile Leu Trp Cys Phe Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser  
275 280 285  
tac tat cat tat ggc egg aag act gtt cag gtg ata aaa gac tga 1030  
Tyr Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp  
15 290 295 300  
tgaaagtcat ccctcaactgt tagtaaggaa gcagtataaca tcaatggaa caggcccat 1090  
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aactgtgtca tcaaaattta agtaatgtgc attgaaaata aggttgatca tggaaatgt 1210  
cagaatttcc aatgtattti taaataaaaa taaaattgtt atttag 1256  
20  
  
(210) 28  
(211) 301

Met Leu Ala Leu Arg Val Ala Arg Gly Ser Trp Gly Ala Leu Arg  
1 5 10 15

Gly Ala Ala Trp Ala Pro Gly Thr Arg Pro Ser Lys Arg Arg Ala Cys  
20 25 30

5 Trp Ala Leu Leu Pro Pro Val Pro Cys Cys Leu Gly Cys Leu Ala Glu  
35 40 45

Arg Trp Arg Leu Arg Pro Ala Ala Leu Gly Leu Arg Leu Pro Gly Ile  
50 55 60

Gly Gln Arg Asn His Cys Ser Gly Ala Gly Lys Ala Ala Pro Arg Pro  
10 65 70 75

Ala Ala Gly Ala Gly Ala Ala Glu Ala Pro Gly Gly Gln Trp Gly  
80 85 90 95

Pro Ala Ser Thr Pro Ser Leu Tyr Glu Asn Pro Trp Thr Ile Pro Asn  
100 105 110

15 Met Leu Ser Met Thr Arg Ile Gly Leu Ala Pro Val Leu Gly Tyr Leu  
115 120 125

Ile Ile Glu Glu Asp Phe Asn Ile Ala Leu Gly Val Phe Ala Leu Ala  
130 135 140

Gly Leu Thr Asp Leu Leu Asp Gly Phe Ile Ala Arg Asn Trp Ala Asn  
20 145 150 155

Gln Arg Ser Ala Leu Gly Ser Ala Leu Asp Pro Leu Ala Asp Lys Ile  
160 165 170 175

Leu Ile Ser Ile Leu Tyr Val Ser Leu Thr Tyr Ala Asp Leu Ile Pro

210                    215                    220  
Ala Lys Tyr Phe Asn Pro Cys Tyr Ala Thr Ala Arg Leu Lys Pro Thr  
225                    230                    235  
Phe Ile Ser Lys Val Asn Thr Ala Val Gln Leu Ile Leu Val Ala Ala  
5      240                    245                    250                    255  
Ser Leu Ala Ala Pro Val Phe Asn Tyr Ala Asp Ser Ile Tyr Leu Gln  
260                    265                    270  
Ile Leu Trp Cys Phe Thr Ala Phe Thr Thr Ala Ala Ser Ala Tyr Ser  
275                    280                    285  
10      Tyr Tyr His Tyr Gly Arg Lys Thr Val Gln Val Ile Lys Asp  
290                    295                    300

&lt;210&gt; 29

15      &lt;211&gt; 1305

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 29

20      tttttttcc ggcgggtccc c atg gag gcg ctg ggg aag ctg aag ctc ttc      51  
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gat gac tac ccc aag act ttg gag gat ttc egg gtc aag aac tgc ggg      99

44 - 45 - 46 - 47 - 48 - 49 - 50 - 51 - 52 - 53 - 54 - 55 - 56 - 57 - 58 - 59 - 60 - 61 - 62 - 63 - 64 - 65 - 66 - 67 - 68 - 69 - 70 - 71 - 72 - 73 - 74 - 75 - 76 - 77 - 78 - 79 - 80 - 81 - 82 - 83 - 84 - 85 - 86 - 87 - 88 - 89 - 90 - 91 - 92 - 93 - 94 - 95 - 96 - 97 - 98 - 99 - 100 - 101 - 102 - 103 - 104 - 105 - 106 - 107 - 108 - 109 - 110 - 111 - 112 - 113 - 114 - 115 - 116 - 117 - 118 - 119 - 120 - 121 - 122 - 123 - 124 - 125 - 126 - 127 - 128 - 129 - 130 - 131 - 132 - 133 - 134 - 135 - 136 - 137 - 138 - 139 - 140 - 141 - 142 - 143 - 144 - 145 - 146 - 147

30                   35                   40  
ctg tcc gag ctg cag tat tac ctc acc acg gag gtg cat cct gag ctc       195  
Leu Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu  
  
45                   50                   55  
5 tac gtg gac aag tcc cgg gga gat aaa ctg aag atc aac atc gat gta       243  
Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val  
  
60                   65                   70  
ctt ttt ccc ccc atg ccc tgt gcc tat ctg agt att gat gcc atg gat       291  
Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp  
  
10      75                   80                   85                   90  
gtg gcc gga gaa cag cag ctg gat gtg gaa ccc aac ctg tcc aag ccc       339  
Val Ala Gly Glu Gln Gln Leu Asp Val Glu His Asn Leu Phe Lys Gln  
  
95                   100                   105  
cga ccc gat aaa gat ggc atc ccc gtg agc tcc gag gct gag cgg cat       387  
15 Arg Leu Asp Lys Asp Gly Ile Pro Val Ser Ser Glu Ala Glu Arg His  
  
110                   115                   120  
gag ctt ggg aaa gtc gag gtg acg gtg ttt gac ccc gac tcc ctg gac       435  
Glu Leu Gly Lys Val Glu Val Thr Val Phe Asp Pro Asp Ser Leu Asp  
  
125                   130                   135  
20 ccc gat ccc tgg gag acg tgc tat ggt gct gag gca gaa gat atc aag       483  
Pro Asp Arg Cys Glu Ser Cys Tyr Gly Ala Glu Ala Asp Ile Lys  
  
140                   145                   150  
tgc tgg acg acg tgt gaa gat gtg cgg gag gca tat cgg cgt aga ggc       531  
  
tgg g                   tgg acg acg gat acg ttt gag cgg tgg cgg cgg gag ggc       579

175                    180                    185  
ttc agc cag aag atg cag gag cag aag aat gaa ggc tgc cag gtg tat        627  
Phe Ser Gln Lys Met Gln Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr  
190                    195                    200  
5    ggc ttc ttg gaa gtc aat aag gtg gcc gga aac ttc cac ttt gcc cct        675  
Gly Phe Leu Glu Val Asn Lys Val Ala Gly Asn Phe His Phe Ala Pro  
205                    210                    215  
ggg aag agc ttc cag cag tcc cat gtg cac gtc cat gac ttg cag agc        723  
Gly Lys Ser Phe Gln Gln Ser His Val His Val His Asp Leu Gln Ser  
10      220                    225                    230  
ttt ggc ctt gac aac atc aac atg acc cac tac atc cag cac ctg tca        771  
Phe Gly Leu Asp Asn Ile Asn Met Thr His Tyr Ile Gln His Leu Ser  
235                    240                    245                    250  
ttt ggg gag gac tat cca ggc att gtg aac ccc ctg gac cac acc aat        819  
15    Phe Gly Glu Asp Tyr Pro Gly Ile Val Asn Pro Leu Asp His Thr Asn  
255                    260                    265  
gtc act gcg ccc eaa gcc tcc atg atg ttc cag tac ttt gtg aag gtg        867  
Val Thr Ala Pro Gln Ala Ser Met Met Phe Gln Tyr Phe Val Lys Val  
270                    275                    280  
20    gtg ccc act gtg tac atg aag gtg gac gga gag gta ctg agg aca aat        915  
Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Arg Thr Asn  
285                    290                    295  
cag ttc tat gtg acc aga cat gag aag gtt gcc aat ggg ctg ttg ggc        963  
gac ccc ggt ttg ccc gga gtt ttc gtt aat ttt gag ttt tgg aat atg        1011

315                   320                   325                   330  
atg gtg aag ctg acg gag aag cac agg tcc ttc acc cac ttc ctg aca       1059       —  
Met Val Lys Leu Thr Glu Lys His Arg Ser Phe Thr His Phe Leu Thr  
  
5                   335                   340                   345  
ggt gtg tgc gcc atc att ggg ggc atg ttc aca gtg gct gga ctc atc       1107  
Gly Val Cys Ala Ile Ile Gly Gly Met Phe Thr Val Ala Gly Leu Ile  
  
10                  350                  355                  360  
gat tcg ctc atc tac cac tca gca cga gcc atc cag aag aaa att gat       1155  
Asp Ser Leu Ile Tyr His Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp  
  
10                  365                  370                  375  
cta ggg aag aca acg tagtcacccct cggtgtttcc tctgttctctt ctttctccct       1210  
Leu Gly Lys Thr Thr  
  
15                  380  
ggcctgttgt tgtccccccag cctctgtccac cctccacccctc ctccgtcage cccagccccca       1270  
gtttgataaaa tctattgatt gatttgtata gtaac       1305

&lt;210&gt; 30

&lt;211&gt; 383

20           212   PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 30

Asp Ala Tyr Pro Iva Ile Ile Ile Asp Phe Arg Val Lys Ile Ile Gly

Gly Ala Thr Val Thr Ile Val Ser Gly Leu Leu Met Leu Leu Phe  
30 35 40  
Leu Ser Glu Leu Gln Tyr Tyr Leu Thr Thr Glu Val His Pro Glu Leu  
45 50 55  
**5** Tyr Val Asp Lys Ser Arg Gly Asp Lys Leu Lys Ile Asn Ile Asp Val  
60 65 70  
Leu Phe Pro His Met Pro Cys Ala Tyr Leu Ser Ile Asp Ala Met Asp  
75 80 85 90  
Val Ala Gly Glu Gln Gln Leu Asp Val Glu His Asn Leu Phe Lys Gln  
**10** 95 100 105  
Arg Leu Asp Lys Asp Gly Ile Pro Val Ser Ser Glu Ala Glu Arg His  
110 115 120  
Glu Leu Gly Lys Val Glu Val Thr Val Phe Asp Pro Asp Ser Leu Asp  
125 130 135  
**15** Pro Asp Arg Cys Glu Ser Cys Tyr Gly Ala Glu Ala Glu Asp Ile Lys  
140 145 150  
Cys Cys Asn Thr Cys Glu Asp Val Arg Glu Ala Tyr Arg Arg Arg Gly  
155 160 165 170  
Trp Ala Phe Lys Asn Pro Asp Thr Ile Glu Gln Cys Arg Arg Gln Gly  
**20** 175 180 185  
Phe Ser Gln Lys Met Gln Glu Gln Lys Asn Glu Gly Cys Gln Val Tyr  
190 195 200  
Gly Phe Leu Glu Val Asn Lys Val Ala Gly Asn Phe His Phe Ala Pro

235                    240                    245                    250  
Phe Gly Glu Asp Tyr Pro Gly Ile Val Asn Pro Leu Asp His Thr Asn  
                       255                    260                    265  
Val Thr Ala Pro Gln Ala Ser Met Met Phe Gln Tyr Phe Val Lys Val  
5                    270                    275                    280  
Val Pro Thr Val Tyr Met Lys Val Asp Gly Glu Val Leu Arg Thr Asn  
                      285                    290                    295  
Gln Phe Ser Val Thr Arg His Glu Lys Val Ala Asn Gly Leu Leu Gly  
                      300                    305                    310  
10 Asp Gln Gly Leu Pro Gly Val Phe Val Leu Tyr Glu Leu Ser Pro Met  
                      315                    320                    325                    330  
Met Val Lys Leu Thr Glu Lys His Arg Ser Phe Thr His Phe Leu Thr  
                      335                    340                    345  
Gly Val Cys Ala Ile Ile Gly Gly Met Phe Thr Val Ala Gly Leu Ile  
15                    350                    355                    360  
Asp Ser Leu Ile Tyr His Ser Ala Arg Ala Ile Gln Lys Lys Ile Asp  
                      365                    370                    375  
Leu Gly Lys Thr Thr  
                      380  
20

&lt;210&gt; 31

&lt;211&gt; 899

cgtcggtgac ctgtggact cggatattc ctgcagctca gcagacccac tggccgtggc 60  
agacttctgc gtt atg acc egg ctg ctg ggc tac gtg gac ccc ctg gat 109  
Met Thr Arg Leu Leu Gly Tyr Val Asp Pro Leu Asp  
1 5 10

5 ccc agc ttt gtg get gcc gtc atc acc atc acc ttc aat ccg etc tac 157  
Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr  
15 20 25  
tgg aat gtg gtt gca cga tgg gaa cac aag acc cgc aag ctg agc agg 205  
Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg  
10 30 35 40  
gcc ttc gga tcc ccc tac ctg gcc tgc tac tct cta agc gtc acc atc 253  
Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile  
45 50 55 60  
ctg ctc ctg aac ttc ctg cgc tcc cac tgc ttc acg cag gcc atg ctg 301  
15 Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu  
65 70 75  
age cag ccc agg atg gag age ctg gac acc ccc geg gcc tac agc ctg 349  
Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu  
80 85 90  
20 ggc ctt gcg ctc ctg gga ctg ggc gtc gtg ctc ggg atc ttt aat tt 397  
Gly Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Ser Ser Phe  
95 100 105  
ttt gaa ctg ggg ttc get gga act ttc cta ggt gat tac ttc ggg atc 445

125                    130                    135                    140  
ccc atg tac tgg gga agc aca gcc aac tac ctg ggc tgg gcc atc atg        541  
Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met  
145                    150                    155  
5 cac gcc agc ccc acg ggc ctg ctc ctg acg gtg ctg gtg gcc ctc acc        589  
His Ala Ser Pro Thr Gly Leu Leu Leu Thr Val Leu Val Ala Leu Thr  
160                    165                    170  
tac ata gtg gct ctc cta tac gaa gag ccc ttc acc get gag atc tac        637  
Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr  
10                    175                    180                    185  
10 cg<sup>g</sup> cag aaa gec tcc ggg tcc cac aag agg agc tgattgagct gcaacagctt        690  
Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser  
190                    195  
tgctgaaggc ctggccagcc tccctggccctg ccccaagtgg cagggccctgc gcagggcgag        750  
15 aatggtgccct gctgtccagg gtcgtcccccc ggctgtggct gccccagtgc cttggAACCT        810  
gttgtccctgg ggaccctgga cgtgccgaca tatggccatt gagctccaac ccacacatcc        870  
ccatccacca ataaaggcac cctgaccctt        899  
  
20                    210 > 32  
<211> 199  
<212> PRT  
<213> Homo sapiens

Pro Ser Phe Val Ala Ala Val Ile Thr Ile Thr Phe Asn Pro Leu Tyr  
15 20 25  
Trp Asn Val Val Ala Arg Trp Glu His Lys Thr Arg Lys Leu Ser Arg  
30 35 40  
**5** Ala Phe Gly Ser Pro Tyr Leu Ala Cys Tyr Ser Leu Ser Val Thr Ile  
45 50 55 60  
Leu Leu Leu Asn Phe Leu Arg Ser His Cys Phe Thr Gln Ala Met Leu  
65 70 75  
Ser Gln Pro Arg Met Glu Ser Leu Asp Thr Pro Ala Ala Tyr Ser Leu  
**10** 80 85 90  
Gly Leu Ala Leu Leu Gly Leu Gly Val Val Leu Val Leu Ser Ser Phe  
95 100 105  
Phe Ala Leu Gly Phe Ala Gly Thr Phe Leu Gly Asp Tyr Phe Gly Ile  
110 115 120  
**15** Leu Lys Glu Ala Arg Val Thr Val Phe Pro Phe Asn Ile Leu Asp Asn  
125 130 135 140  
Pro Met Tyr Trp Gly Ser Thr Ala Asn Tyr Leu Gly Trp Ala Ile Met  
145 150 155  
His Ala Ser Pro Thr Gly Leu Leu Ile Thr Val Leu Val Ala Ile Thr  
**20** 160 165 170  
Tyr Ile Val Ala Leu Leu Tyr Glu Glu Pro Phe Thr Ala Glu Ile Tyr  
175 180 185  
Arg Gln Lys Ala Ser Gly Ser His Lys Arg Ser

&lt;211&gt; 905

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

5 &lt;400&gt; 33

aacggaaa atg geg cct cac ggc ccg ggt agt ctt acg acc ctg gtg ccc 50

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro

1 5 10

tgg gct gcc gcc ctg ctc get ctg ggc gtg gaa agg get ctg geg 98

10 Trp Ala Ala Ala Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala

15 20 25 30

cta ccc gag ata tgc acc cua tgt cca ggg agc gtg caa aat ttg tca 146

Leu Pro Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn Leu Ser

35 40 45

15 aaa gtg gcc ttt tat tgt aaa acg aca cga gag cta arg ctg cat gcc 194

Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala

50 55 60

tgt tgt tgc ctg aat cag aag ggc acc ate ttg ggg ctg gat ctc cag 242

Arg Cys Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln

20 65 70 75

aac tgt tct ctg gag gac cct ggt cca aac ttt cat cag gca cat acc 290

Asn Cys Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr

80 85 90

	Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln		
	115	120	125
	cat gtc aac tgt cct gga gga att aat gcc tgg aat act atc aac tct		43-
	His Val Asn Cys Pro Gly Gly Ile Asn Ala Trp Asn Thr Ile Thr Ser		
5	130	135	140
	tat ata gac aac caa atc tgt caa ggg caa aag aac ctt tgc aat aac		482
	Tyr Ile Asp Asn Gln Ile Cys Gln Gly Gln Lys Asn Leu Cys Asn Asn		
	145	150	155
	act ggg gac cca gaa atg tgt cct gag aat gga tct tgt gta cct gat		530
10	Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp		
	160	165	170
	ggt cca ggt ctt ttg cag tgt gtt tgt get gat ggt ttc cat gga tac		578
	Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr		
	175	180	185
	190		
15	aag tgt atg cgc cag ggc tgg ttc tca ctg ctt atg ttc ttc ggg att		626
	Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile		
	195	200	205
	ctg gga gcc acc act cta tcc gtc tcc att ctg ctt tgg geg acc cag		674
	Leu Gly Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln		
20	210	215	220
	cgc cga aaa gcc aag act tca tggaa tacataggte ttaccatttgaa		720
	Arg Arg Lys Ala Lys Thr Ser		

<sup>1</sup> See also the discussion of the relationship between the two concepts in the introduction to this volume.

1210> 34

1211> 229

5 212> PRT

213> Homo sapiens

400> 34

Met Ala Pro His Gly Pro Gly Ser Leu Thr Thr Leu Val Pro

10 1 5 10

Trp Ala Ala Ala Leu Leu Leu Ala Leu Gly Val Glu Arg Ala Leu Ala

15 20 25 30

Leu Pro Glu Ile Cys Thr Gln Cys Pro Gly Ser Val Gln Asn Leu Ser

35 40 45

15 Lys Val Ala Phe Tyr Cys Lys Thr Thr Arg Glu Leu Met Leu His Ala

50 55 60

Arg Cys Cys Leu Asn Gln Lys Gly Thr Ile Leu Gly Leu Asp Leu Gln

65 70 75

Asn Cys Ser Leu Glu Asp Pro Gly Pro Asn Phe His Gln Ala His Thr

20 80 85 90

Thr Val Ile Ile Asp Leu Gln Ala Asn Pro Ile Lys Gly Asp Leu Ala

95 100 105 110

Asn Thr Phe Arg Gly Phe Thr Gln Leu Gln Thr Leu Ile Leu Pro Gln

	145	150		155
	Thr Gly Asp Pro Glu Met Cys Pro Glu Asn Gly Ser Cys Val Pro Asp			
	160	165		170
	Gly Pro Gly Leu Leu Gln Cys Val Cys Ala Asp Gly Phe His Gly Tyr			
5	175	180	185	190
	Lys Cys Met Arg Gln Gly Ser Phe Ser Leu Leu Met Phe Phe Gly Ile			
	195	200		205
	Leu Gly Ala Thr Thr Leu Ser Val Ser Ile Leu Leu Trp Ala Thr Gln			
	210	215		220
10	Arg Arg Lys Ala Lys Thr Ser			
	225			

210 35

15 (211) 841

212 DNA

(213) *Homo sapiens*

400. 35

Met. San. Rue. San. 20. Aug.  
20 ttcacggagg ctgegggtt aggacccca gtcggatc atg tag cttt ttt ggt cgc 56

ctg tgt ctt ctc acc ate gtt ggc ctg att ctc ccc acc aga gga cag 164

25                   30                   35  
gac att cag gtc ccc aca ega gcc cca gat gca gtc tac aca gaa ctc       200  
Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu  
40                   45                   50  
5    eag ccc acc tct cca acc cca acc tgg cct get gat gaa aca aca caa       248  
Gln Pro Thr Ser Pro Thr Pro Trp Pro Ala Asp Glu Thr Pro Gln  
55                   60                   65                   70  
ccc eag acc eag acc eag cca ctg gaa gga aeg gat ggg cct cta gtg       296  
Pro Gln Thr Gln Thr Gln Gln Leu Glu Gly Thr Asp Gly Pro Leu Val  
10                   75                   80                   85  
10                   75                   80                   85  
aca gat cca gag aca cac aag agc acc aaa gca get cat ccc act gat       344  
Thr Asp Pro Glu Thr His Lys Ser Thr Lys Ala Ala His Pro Thr Asp  
90                   95                   100  
gac acc aeg acg ctc tct gag aga cca tcc cca agc aca gac gtc cag       392  
15    Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln  
105                  110                  115  
aca gac ccc eag acc ctc aag cca tct ggt ttt cat gag gat gac ccc       440  
Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro  
120                  125                  130  
20    ttc ttc tat gat gaa cac acc ctc egg aad egg ggg ctg ttg gtc gca       488  
Phe Phe Tyr Asp Glu His Thr Leu Arg Lys Arg Gly Leu Leu Val Ala  
135                  140                  145                  150  
get gtg ctg ttc atc aca ggc atc atc atc ctc acc agt ggc aug tgc       536  
agg ccc ctg ttc egg ttg ttg egg dtt ttg agg tggtt       586

170 175

tcagaaacag gagctgacaa cccgctggc acccgaagac caagccccct gccagctcac 640  
cgtccccaggc ctccctgcata ccctcgaga gcctggccag agagggaaga cacagatgat 700  
gaagctggag ccagggctgc cggtccgagt ctccctaccct ccccaaccct gcccggccct 760  
5 gaaggctacc tggcgccttg ggggctgtcc ctcaagttat ctccctgtt aagacaaaaa 820  
gtaaagcaact gtggctttg c 841

&lt;210&gt; 36

10 &lt;211&gt; 178

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

15 Met Ser Pro Ser Gly Arg

1 5

Leu Cys Leu Leu Thr Ile Val Gly Leu Ile Leu Pro Thr Arg Gly Gln

10 15 20

Thr Leu Lys Asp Thr Thr Ser Ser Ser Ser Ala Asp Ser Thr Ile Met

20 25 30 35

Asp Ile Gln Val Pro Thr Arg Ala Pro Asp Ala Val Tyr Thr Glu Leu

40 45 50

Gln Pro Thr Ser Pro Thr Pro Trp Pro Ala Asp Glu Thr Pro Gln

75

80

85

	90	95	100
	Asp Thr Thr Thr Leu Ser Glu Arg Pro Ser Pro Ser Thr Asp Val Gln		
	105	110	115
	Thr Asp Pro Gln Thr Leu Lys Pro Ser Gly Phe His Glu Asp Asp Pro		
5	120	125	130
	Phe Phe Tyr Asp Glu His Thr Leu Arg Lys Arg Gly Leu Leu Val Ala		
	135	140	145
	Ala Val Leu Phe Ile Thr Gly Ile Ile Ile Leu Thr Ser Gly Lys Cys		
	155	160	165
10	Arg Gln Leu Ser Arg Leu Cys Arg Asn His Cys Arg		
	170	175	

210 · 37

15 211 · 1451

· 212 · DNA

213 Homo sapiens

400 37

Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro  
25 30 35

gcc ggg tcc ccg cgg ggc ctc agg aag ggg gcg gcc ccc gcg cgg gag 260  
Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu  
5 40 45 50

aga cgc ggc cga gaa cag tcc act ttg gaa agt gaa gaa tgg aat cct 308  
Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro  
55 60 65

tgg gaa gga gat gaa aaa aat gag caa caa cac aga ttt aaa aet age 356  
10 Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser  
70 75 80

ctt caa ata tta gat aaa tcc acg aaa gga aaa aca gat ctc agt gta 404  
Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val  
85 90 95 100

caa atc tgg ggc aaa gct gcc att ggc ttg tat ctc tgg gag cat att 452  
15 Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile  
105 110 115

ttt gaa ggc tta ctt gat ccc agc gat gtg act gct caa tgg aga gaa 500  
Phe Glu Gly Leu Leu Asp Pro Ser Asp Val Thr Ala Gln Trp Arg Glu  
20 120 125 130

gga aag tca atc gta gga aga aca cag tac agc ttc atc aet ggt eca 548  
Gly Lys Ser Ile Val Gly Arg Thr Gln Tyr Ser Phe Ile Thr Gly Pro  
135 140 145

ile leu asn gly arg glu lys ala lys ile phe tyr ala thr gln trp  
165 170 175 180  
tta ctt tat gca caa aat tta gtg caa att caa aaa ctc cag cat ctt 692  
Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu  
5 185 190 195  
gct gtt gtt ttg ctc gga aat gaa cat tgt gat aat gag tgg ata aac 740  
Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn  
200 205 210  
cca ttc ctc aaa aga aat gga ggc ttc gtg gag ctg ctt ttc ata ata 788  
10 Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu Leu Phe Ile Ile  
215 220 225  
tat gac agc ccc tgg att aat gac gtg gat gtt ttt cag tgg cct tta 836  
Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu  
230 235 240  
15 gga gta gca aca tac agg aat ttt cct gtg gtg gag gca agt tgg tca 884  
Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser  
245 250 255 260  
atg ctg cat gat gag agg cca tat tta tgt aat ttc tta ggu acg att 932  
Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile  
20 265 270 275  
tat gaa aat tca tcc aga cag gca cta atg aac att ttg aaa aaa gat 980  
Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp  
280 285 290

Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln  
310 315 320  
agt gat ctc aca ttg tgc ccg gtc gga gta aac aca gaa tgc tat cga 1124  
Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg  
5 325 330 335 340  
atc tat gag gct tgc tcc tat ggc tcc att cct gtg gtg gaa gac gtg 1172  
Ile Tyr Glu Ala Cys Ser Tyr Gly Ser Ile Pro Val Val Glu Asp Val  
345 350 355  
atg aca gct ggc aac tgt ggg aat aca tct gtg cac cac ggt gct cct 1220  
10 Met Thr Ala Gly Asn Cys Gly Asn Thr Ser Val His His Gly Ala Pro  
360 365 370  
ctg cag tta ctc aag tcc atg ggt gct ccc ttt atc ttt atc aag aac 1268  
Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn  
375 380 385  
15 tgg aag gaa ctc cct gct gtt tta gaa aaa gag aaa act ata att tta 1316  
Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu  
390 395 400  
caa gaa aaa att gaa aga aga aaa atg tta ctt cag tgg tat cag cae 1364  
Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His  
20 405 410 415 420  
ttc aag aca gag ctt aaa atg aaa ttt act aat att tta gaa agc tca 1412  
Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser  
425 430 435

<210> 38  
211 > 443  
· 212 > PRT  
5 · 213 > Homo sapiens

<400> 38

Met Arg Leu Thr  
1

10 Arg Lys Arg Leu Cys Ser Phe Leu Ile Ala Leu Tyr Cys Leu Phe Ser  
5 10 15 20

Leu Tyr Ala Ala Tyr His Val Phe Phe Gly Arg Arg Arg Gln Ala Pro  
25 30 35

Ala Gly Ser Pro Arg Gly Leu Arg Lys Gly Ala Ala Pro Ala Arg Glu  
15 40 45 50

Arg Arg Gly Arg Glu Gln Ser Thr Leu Glu Ser Glu Glu Trp Asn Pro  
55 60 65

Trp Glu Gly Asp Glu Lys Asn Glu Gln Gln His Arg Phe Lys Thr Ser  
70 75 80

20 Leu Gln Ile Leu Asp Lys Ser Thr Lys Gly Lys Thr Asp Leu Ser Val  
85 90 95 100

Gln Ile Trp Gly Lys Ala Ala Ile Gly Leu Tyr Leu Trp Glu His Ile  
105 110 115

Gly Lys Ser Ile Val Asp Arg Ile Gln Ile Ser Ile Ile Thr Asp Ile

Ala Val Ile Pro Gly Tyr Phe Ser Val Asp Val Asn Asn Val Val Leu  
150 155 160

Ile Leu Asn Gly Arg Glu Lys Ala Lys Ile Phe Tyr Ala Thr Gln Trp  
165 170 175 180

5 Leu Leu Tyr Ala Gln Asn Leu Val Gln Ile Gln Lys Leu Gln His Leu  
185 190 195

Ala Val Val Leu Leu Gly Asn Glu His Cys Asp Asn Glu Trp Ile Asn  
200 205 210

Pro Phe Leu Lys Arg Asn Gly Gly Phe Val Glu Leu Leu Phe Ile Ile  
10 215 220 225

Tyr Asp Ser Pro Trp Ile Asn Asp Val Asp Val Phe Gln Trp Pro Leu  
230 235 240

Gly Val Ala Thr Tyr Arg Asn Phe Pro Val Val Glu Ala Ser Trp Ser  
245 250 255 260

15 Met Leu His Asp Glu Arg Pro Tyr Leu Cys Asn Phe Leu Gly Thr Ile  
265 270 275

Tyr Glu Asn Ser Ser Arg Gln Ala Leu Met Asn Ile Leu Lys Lys Asp  
280 285 290

Gly Asn Asp Lys Leu Cys Trp Val Ser Ala Arg Glu His Trp Gln Pro  
20 295 300 305

Gln Glu Thr Asn Glu Ser Leu Lys Asn Tyr Gln Asp Ala Leu Leu Gln  
310 315 320

Ser Asp Leu Thr Leu Cys Pro Val Gly Val Asn Thr Glu Cys Tyr Arg  
330 335 340

345 350 355

360

365

370

Leu Gln Leu Leu Lys Ser Met Gly Ala Pro Phe Ile Phe Ile Lys Asn

375

380

385

Trp Lys Glu Leu Pro Ala Val Leu Glu Lys Glu Lys Thr Ile Ile Leu

5

390

395

400

Gln Glu Lys Ile Glu Arg Arg Lys Met Leu Leu Gln Trp Tyr Gln His

405

410

415

420

Phe Lys Thr Glu Leu Lys Met Lys Phe Thr Asn Ile Leu Glu Ser Ser

425

430

435

10 Phe Leu Met Asn Asn Lys Ser

440

&lt;210&gt; 39

15 &lt;211&gt; 886

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

20 accaaacatg tggacgcggc cccggggacgg ccgttgtggatg gctgtgtggat cactcgacgg 60

tc atg gag acc ctg ggg gca ctt ctg gtg ctg gag ttt ctg ctc ctc 107

Met Glu Thr Leu Glv Ala Leu Leu Val Leu Glu Phe Leu Leu Leu

1

5

10

15

20

25

30

Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu

35 40

13

gtc tgg ctg gcc aac cgc ctc tgg tgt tcc aag gcc agg gct gag gac 251

Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp

5 50 55 60

gag gag gag acc acg ttc aga atg gag tcc aac cta tac cag gac cag 299

Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln

65 70 75 80 85 90 95

agt gaa gac aag aga gag aag aaa gag gag gcc aag gag aua gaa gag aag

10 Ser Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys

80                    85                    90                    95

agg aag aag gag aaa aag aca gca aag gaa gga gag agc aac ttg gga 395

Arg Lys Lys Glu Lys Lys Thr Ala Lys Glu Glu Glu Glu Ser Asp Leu Gly

100                  105                  110

15 ctg gat ctg gag aaa gag ccc gga gac cat gag aya uca aag aco

[Leu-Asp-Leu-Glu-Glu-Lys-Glu-Pro-Gly-Asp-His-Glu-Arg-Ala-Lys-Ser]

115                    120                    125

aca gtc atg tgaatgtt cctggcgcc tcgtttccaggc agtcccccaat ugttgtttat

The Met

136

— 3 —

*Argyresthia goedartella* (guadalupe) *Argyresthia decolorata* (colorado) *Argyresthia* 620

getcttggg taadatggc tccatgcac ccccttcctt gagttttggcc ttgttgttggc 680

Lehrveranstaltung für den ersten und zweiten Studienjahr. Inhalt: Die Theorie des Stochastischen Prozesses.

210 40

211 130

5 212 PRT

213 Homo sapiens

400 40

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu

10 1 5 10 15

Ser Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp

20 25 30

Leu Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu

35 40 45

15 Val Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp

50 55 60

Glu Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln

65 70 75

Ser Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys

20 80 85 90 95

Arg Lys Lys Glu Lys Lys Thr Ala Lys Glu Glu Ser Asn Leu Gly

100 105 110

Leu Asp Leu Glu Glu Lys Glu Pro Glv Asp His Glu Arg Ala Lys Ser